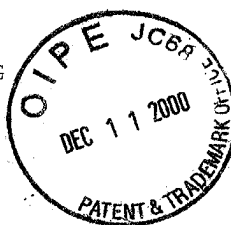


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TECH CENTER 1600/2900

## SEQUENCE LISTING



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TANAKA, Yoshikazu  
KUSUMI, Takaaki  
MIZUTANI, Masako  
NAKAYAMA, Toru

<120> GENE ENCODING PROTEIN HAVING AURONE SYNTHESIZING ACTIVITY

<130> 001560-377

<140> US 09/446,089

<141> 1999-12-17

<150> PCT/JP99/02045

<151> 1999-04-16

<150> JP 10/107296

<151> 1998-04-17

<160> 15

<170> PatentIn version 3.0

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                               Met Phe Lys Asn Pro Asn
                               1           5

atc cgc tat cac aaa cta tct tcc aaa tcc aat gac aac gat caa gaa      161
Ile Arg Tyr His Lys Leu Ser Ser Lys Ser Asn Asp Asn Asp Gln Glu
                               10           15           20

tcc tcc cat cgt tgt aag cac att cta tta ttt ata ata acc tta ttc      209
Ser Ser His Arg Cys Lys His Ile Leu Leu Phe Ile Ile Thr Leu Phe
                               25           30           35

cta ctt ata gtt ggc ctg tac atc gcc aac tct ctc gcc tat gcc cgg      257
Leu Leu Ile Val Gly Leu Tyr Ile Ala Asn Ser Leu Ala Tyr Ala Arg
                               40           45           50

ttt gcc tcg acc tca acc ggc cct atc gcc gcc cct gat gtc acc aaa      305
Phe Ala Ser Thr Ser Thr Gly Pro Ile Ala Ala Pro Asp Val Thr Lys
55           60           65           70

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tgt ggt cag cca gac ttg cca cct ggc aca gcc cca ata aac tgt tgt	353
Cys Gly Gln Pro Asp Leu Pro Pro Gly Thr Ala Pro Ile Asn Cys Cys	
75 80 85	
ccc cca atc ccc gct aaa atc atc gat ttc gag cta cca cct ccc tcc	401
Pro Pro Ile Pro Ala Lys Ile Ile Asp Phe Glu Leu Pro Pro Pro Ser	
90 95 100	
act acc atg agg gtt cgc cgt gcg gct cat tta gtt gat gat gca tac	449
Thr Thr Met Arg Val Arg Arg Ala Ala His Leu Val Asp Asp Ala Tyr	
105 110 115	
att gcc aaa ttc aag aaa gcc gtt gag ctt atg cga gct cta cct gag	497
Ile Ala Lys Phe Lys Lys Ala Val Glu Leu Met Arg Ala Leu Pro Glu	
120 125 130	
gat gac cct cgt agc ttc aag caa caa gct aac gtc cat tgc gct tac	545
Asp Asp Pro Arg Ser Phe Lys Gln Gln Ala Asn Val His Cys Ala Tyr	
135 140 145 150	
tgc gcg ggg gcg tat aat caa gcc ggt ttc aca aac cta aag ctc caa	593
Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe Thr Asn Leu Lys Leu Gln	
155 160 165	
atc cac cga tct tgg ctt ttt ttc ccg ttc cat aga tat tat atc tac	641
Ile His Arg Ser Trp Leu Phe Phe Pro Phe His Arg Tyr Tyr Ile Tyr	
170 175 180	
ttt ttt gaa aga ata ttg gga aaa cta atc aat gat aca act ttt gct	689
Phe Phe Glu Arg Ile Leu Gly Lys Leu Ile Asn Asp Thr Thr Phe Ala	
185 190 195	
ctc caa ttt tgg aac tat gat tca cct ggt gga atg aca atc cca tca	737
Leu Gln Phe Trp Asn Tyr Asp Ser Pro Gly Gly Met Thr Ile Pro Ser	
200 205 210	
atg ttt att gat act aat tct tcg ctg tac gat agt tta cgg gac agt	785
Met Phe Ile Asp Thr Asn Ser Ser Leu Tyr Asp Ser Ser Leu Arg Asp Ser	
215 220 225 230	
aat cat cag cca cca acc atc gta gac ttg aac tac gcc ttt tct gat	833
Asn His Gln Pro Pro Thr Ile Val Asp Leu Asn Tyr Ala Phe Ser Asp	
235 240 245	
tcc gac aat acc act act cct gaa gag caa atg att ata aac ctt aaa	881
Ser Asp Asn Thr Thr Thr Pro Glu Glu Gln Met Ile Ile Asn Leu Lys	
250 255 260	
att gtg tac aga caa atg gtg tcg agc gct aag act cca cag ctt ttc	929
Ile Val Tyr Arg Gln Met Val Ser Ser Ala Lys Thr Pro Gln Leu Phe	
265 270 275	
ttc ggc cgc cca tac cga cgt ggg gac caa gag ttt ccc ggg gtg ggg	977
Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln Glu Phe Pro Gly Val Gly	
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Ser Ile Glu Leu Val Pro His Gly Met Ile His Leu Trp Thr Gly Ser	

295	300	305	310	
gag aac acg ccc tat ggc gag aac atg ggg gct ttc tac tca acg gct				1073
Glu Asn Thr Pro Tyr 315	Gly Glu Asn Met 320	Gly Ala Phe Tyr Ser Thr Ala 325		
aga gac ccg ata ttt ttt gct cat cat tcg aac gtc gat aga atg tgg				1121
Arg Asp Pro Ile Phe Phe Ala His His Ser Asn Val Asp Arg Met Trp 330	335	340		
tcc ata tgg aag acc cta gga ggg ccg ccg agg acg gac tta aca gat				1169
Ser Ile Trp Lys Thr Leu Gly 345	Gly Pro Arg Arg Thr 350	Asp Leu Thr Asp 355		
cca gat ttt ctt gat gcg tct ttc gtt ttt tat gac gaa aac gca gag				1217
Pro Asp Phe Leu Asp Ala Ser Phe Val Phe Tyr Asp Glu Asn Ala Glu 360	365	370		
atg gtt ccg gtc aag gtt ccg gat tgc tta gat gaa aag aaa cta ggg				1265
Met Val Arg Val Lys Val Arg Asp Cys Leu Asp Glu Lys Lys Leu Gly 375	380	385		
tac gtt tat caa gat gtg gag att ccg tgg ctc aac act cgt cca aca				1313
Tyr Val Tyr Gln Asp Val Glu Ile Pro Trp Leu Asn Thr Arg Pro Thr 395	400	405		
cca aaa gtt tct ccg tct cta ctt aag aaa ttt cat aga aca aac act				1361
Pro Lys Val Ser Pro Ser Leu Leu Lys Lys Phe His Arg Thr Asn Thr 410	415	420		
gcc aat ccg aga caa gtt ttt cct gcg ata ctt gac aga gtc tta aaa				1409
Ala Asn Pro Arg Gln Val Phe Pro Ala Ile Leu Asp Arg Val Leu Lys 425	430	435		
gtt atc gtg acg agg ccg aag aaa act aga agt agg aaa gaa aag gac				1457
Val Ile Val Thr Arg Pro Lys Lys Thr Arg Ser Arg Lys Glu Lys Asp 440	445	450		
gag tta gaa gag att tta gtg att gaa ggg att gaa ctg gaa aga gac				1505
Glu Leu Glu Glu Ile Leu Val Ile Glu Gly Ile Glu Leu Glu Arg Asp 455	460	465		
cac ggg cac gta aaa ttc gac gtt tat att aat gct gac gaa gat gac				1553
His Gly His Val Lys Phe Asp Val Tyr Ile Asn Ala Asp Glu Asp Asp 475	480	485		
ctt gcg gtg att tcg ccg gag aat gct gag ttc gcc ggg agt ttc gtg				1601
Leu Ala Val Ile Ser Pro Glu Asn Ala Glu Phe Ala Gly Ser Phe Val 490	495	500		
agt ctg tgg cac aaa cct ata aag ggg aag agg aca aag acg cag tta				1649
Ser Leu Trp His Lys Pro Ile Lys Gly Lys Arg Thr Lys Thr Gln Leu 505	510	515		
tta aca ttg tcg att tgt gat att ttg gag gat ttg gat gct gac gaa				1697
Leu Thr Leu Ser Ile Cys Asp Ile Leu Glu Asp Leu Asp Ala Asp Glu 520	525	530		

gat gat tat gtg ttg gtc act ttg gtt ccg aga aac gcc gga gat gcg 1745  
 Asp Asp Tyr Val Leu Val Thr Leu Val Pro Arg Asn Ala Gly Asp Ala  
 535 540 545 550

atc aag att cat aat gtc aag att gag ctt gat ggc taataaattc 1791  
 Ile Lys Ile His Asn Val Lys Ile Glu Leu Asp Gly  
 555 560

tattgatttc ttctcaacct acagttgatc atttaccgat tgattattcc aataaaagta 1851

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<211> 562

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<400> 2

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Asn Asp Asn Asp Gln Glu Ser Ser His Arg Cys Lys His Ile Leu Leu  
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Phe Ile Ile Thr Leu Phe Leu Leu Ile Val Gly Leu Tyr Ile Ala Asn  
 35 40 45

Ser Leu Ala Tyr Ala Arg Phe Ala Ser Thr Ser Thr Gly Pro Ile Ala  
 50 55 60

Ala Pro Asp Val Thr Lys Cys Gly Gln Pro Asp Leu Pro Pro Gly Thr  
 65 70 75 80

Ala Pro Ile Asn Cys Cys Pro Pro Ile Pro Ala Lys Ile Ile Asp Phe  
 85 90 95

Glu Leu Pro Pro Pro Ser Thr Thr Met Arg Val Arg Arg Ala Ala His  
 100 105 110

Leu Val Asp Asp Ala Tyr Ile Ala Lys Phe Lys Lys Ala Val Glu Leu  
 115 120 125

Met Arg Ala Leu Pro Glu Asp Asp Pro Arg Ser Phe Lys Gln Gln Ala  
 130 135 140

Asn Val His Cys Ala Tyr Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe  
 145 150 155 160

Thr Asn Leu Lys Leu Gln Ile His Arg Ser Trp Leu Phe Phe Pro Phe  
 165 170 175

His Arg Tyr Tyr Ile Tyr Phe Phe Glu Arg Ile Leu Gly Lys Leu Ile  
 180 185 190

Asn Asp Thr Thr Phe Ala Leu Gln Phe Trp Asn Tyr Asp Ser Pro Gly  
 195 200 205

Gly Met Thr Ile Pro Ser Met Phe Ile Asp Thr Asn Ser Ser Leu Tyr  
 210 215 220

Asp Ser Leu Arg Asp Ser Asn His Gln Pro Pro Thr Ile Val Asp Leu  
 225 230 235 240

Asn Tyr Ala Phe Ser Asp Ser Asp Asn Thr Thr Thr Pro Glu Glu Gln  
 245 250 255

Met Ile Ile Asn Leu Lys Ile Val Tyr Arg Gln Met Val Ser Ser Ala  
 260 265 270

Lys Thr Pro Gln Leu Phe Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln  
 275 280 285

Glu Phe Pro Gly Val Gly Ser Ile Glu Leu Val Pro His Gly Met Ile  
 290 295 300

His Leu Trp Thr Gly Ser Glu Asn Thr Pro Tyr Gly Glu Asn Met Gly  
 305 310 315 320

Ala Phe Tyr Ser Thr Ala Arg Asp Pro Ile Phe Phe Ala His His Ser  
 325 330 335

Asn Val Asp Arg Met Trp Ser Ile Trp Lys Thr Leu Gly Gly Pro Arg  
 340 345 350

Arg Thr Asp Leu Thr Asp Pro Asp Phe Leu Asp Ala Ser Phe Val Phe  
 355 360 365

Tyr Asp Glu Asn Ala Glu Met Val Arg Val Lys Val Arg Asp Cys Leu  
 370 375 380

Asp Glu Lys Lys Leu Gly Tyr Val Tyr Gln Asp Val Glu Ile Pro Trp  
 385 390 395 400

Leu Asn Thr Arg Pro Thr Pro Lys Val Ser Pro Ser Leu Leu Lys Lys  
 405 410 415

Phe His Arg Thr Asn Thr Ala Asn Pro Arg Gln Val Phe Pro Ala Ile  
 420 425 430

Leu Asp Arg Val Leu Lys Val Ile Val Thr Arg Pro Lys Lys Thr Arg  
 435 440 445

Ser Arg Lys Glu Lys Asp Glu Leu Glu Glu Ile Leu Val Ile Glu Gly  
 450 455 460

Ile Glu Leu Glu Arg Asp His Gly His Val Lys Phe Asp Val Tyr Ile  
 465 470 475 480

Asn Ala Asp Glu Asp Asp Leu Ala Val Ile Ser Pro Glu Asn Ala Glu  
 485 490 495

Phe Ala Gly Ser Phe Val Ser Leu Trp His Lys Pro Ile Lys Gly Lys  
 500 505 510

Arg Thr Lys Thr Gln Leu Leu Thr Leu Ser Ile Cys Asp Ile Leu Glu  
 515 520 525

Asp Leu Asp Ala Asp Glu Asp Asp Tyr Val Leu Val Thr Leu Val Pro  
 530 535 540

Arg Asn Ala Gly Asp Ala Ile Lys Ile His Asn Val Lys Ile Glu Leu  
 545 550 555 560

Asp Gly

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 <212> PRT  
 <213> Antirrhinum majus

<400> 3

Lys Lys Leu Gly Tyr Val Tyr Gln Asp Val Glu Ile Pro

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<210> 4  
 <211> 12  
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<400> 4

Lys Ile Val Tyr Arg Gln Met Val Ser Ser Ala Lys  
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<210> 5  
 <211> 18  
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<400> 5

Lys Thr Pro Gln Leu Phe Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln  
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Glu Phe

<210> 6  
 <211> 29  
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<220>  
 <221> UNSURE  
 <222> (9)..(9)  
 <223> Amino acid 9 is Xaa wherein Xaa = unknown or other.

<220>  
 <221> UNSURE  
 <222> (29)..(29)  
 <223> Amino acid 29 is Xaa wherein Xaa = unknown or other.

<400> 6

Lys Ile Asp Phe Glu Leu Pro Xaa Pro Ser Thr Thr Met Arg Val Arg  
 1 5 10 15

Arg Ala Ala His Leu Val Asp Asp Ala Tyr Ile Xaa Lys  
 20 25

<210> 7  
 <211> 125  
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<400> 7

Arg Gln Met Val Ser Ser Ala Lys Thr Pro Gln Leu Phe Phe Gly Arg

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Leu Val Pro His Gly Met Ile His Leu Trp Thr Gly Ser Glu Asn Thr	35	40	45
Pro Tyr Gly Glu Asn Met Gly Ala Phe Tyr Ser Thr Ala Arg Asp Pro	50	55	60
Ile Phe Phe Ala His His Ser Asn Val Asp Arg Met Trp Ser Ile Trp	65	70	75
Lys Thr Leu Gly Gly Pro Arg Arg Thr Asp Leu Thr Asp Pro Asp Phe	85	90	95
Leu Asp Ala Ser Phe Val Phe Cys Asp Glu Asn Ala Glu Met Val Arg	100	105	110
Val Lys Val Arg Asp Cys Leu Asp Gly Lys Lys Leu Gly	115	120	125

<210> 8  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <221> PEPTIDE  
 <222> (2)..(2)  
 <223> Amino acid 2 is Xaa wherein Xaa = Val or Ile.

<400> 8

Phe Xaa Lys Phe Thr Ala Ile  
 1 5

<210> 9  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <221> PEPTIDE  
 <222> (6)..(6)  
 <223> Amino acid 6 is Xaa wherein Xaa = Thr or Pro.

<400> 9

Lys Trp Lys Gly Lys Xaa  
 1 5

<210> 10  
 <211> 6  
 <212> PRT



<213> Artificial Sequence

<400> 10

His Ala Val Cys Asn Glu  
1 5

<210> 11

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<221> misc\_feature

<222> (6)..(18)

<223> Nucleotides 6, 15 and 18 are "n" wherein "n" = a or c or g or t/u  
or unknown or other

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ttyrtnaart tyacngcnat

20

<210> 12

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<221> misc\_feature

<222> (12)..(12)

<223> Nucleotide 12 is "n" wherein "n" = a or c or g or t/u or unknown  
or other

<400> 12

aartggaarg gnaarmc

17

<210> 13

<211> 18

<212> DNA

<213> Primer

<220>

<221> misc\_feature

<222> (4)..(7)

<223> Nucleotides 4 and 7 are "n" wherein "n" = a or c or g or t/u or u  
nknown or other

<400> 13

rtgngcnacr carttytc

18

<210> 14

<211> 20

<212> DNA

<213> Primer

<400> 14

aaggatccgg ccctatcgcc

20

<210> 15

<211> 22

<212> DNA

<213> Primer

<400> 15

gggttcgaag aattcatctc tg

22